

SEQUENCE PROTOCOL

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Boehringer Mannheim GmbH
- (B) ROAD: Sandhofer Str. 112-132
- (C) CITY: Mannheim
- (E) COUNTRY: Germany
- (F) POSTAL CODE: 68305

(ii) TITLE OF INVENTION: T cells specific for kidney carcinoma

(iii) NUMBER OF SEQUENCES: 22

(iv) COMPUTER-READABLE FORM:

- (A) DATA CARRIER: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, version # 1.30 (EPA)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1341 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..801

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) POSITION: 1..54

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) POSITION: 55..801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG AGG CAA GTG GCG AGA GTG ATC Met Arg Gln Val Ala Arg Val Ile	GTG TTC CTG ACC CTG AGT ACT TTG Val Phe Leu Thr Leu Ser Thr Leu	48
-18 -15	-10 -5	
AGC CTT GCT AAG ACC ACC CAG CCC Ser Leu Ala Lys Thr Thr Gln Pro	ATC TCC ATG GAC TCA TAT GAA GGA Ile Ser Met Asp Ser Tyr Glu Gly	96
1 5	10	
CAA GAA GTG AAC ATA ACC TGT AGC Gln Glu Val Asn Ile Thr Cys Ser	CAC AAC AAC ATT GCT ACA AAT GAT His Asn Asn Ile Ala Thr Asn Asp	144
15 20	25 30	
TAT ATC ACG TGG TAC CAA CAG TTT Tyr Ile Thr Trp Tyr Gln Gln Phe	CCC AGC CAA GGA CCA CGA TTT ATT Pro Ser Gln Gly Pro Arg Phe Ile	192
35	40 45	

ATT CAA GGA TAC AAG ACA Ile Gln Gly Tyr Lys Thr Val	50	AAA GTT ACA AAC GAA GTG GCG CCC CTG TTT	55	60	240
Ile Pro Ala Asp Arg Lys Ser Ser Lys Ser Thr Leu Ser	65	Arg Val Val Pro Arg Val Ser	70	75	288
CTG AGC GAC ACT GCT Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val	80	Gly 85	Gly 90	Gly Ser Ala Arg	336
CAA CTG ACC TTT GGA Gln Leu Thr Phe Gly Ser Gly Thr Gln	95	TCT GGG ACA CAA TTG ACT GTT TTA CCT GAT ATC	100	105	384
Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser	115	120	125	Ile 110	432
GAC AAC CCT GAC CCT Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val	130	135	140	Asp 480	480
TCA CAA AGT AAG GAT TCT Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu	145	GAT GTG TAT ATC ACA GAC AAA ACT GTG CTA	150	155	528
GAC ATG AGG TCT ATG GAC Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser	160	TTC AAG AGC AAC AGT GCT GTG GCC TGG AGC	165	170	576
AAC AAA TCT GAC TTT GCA Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile	175	TGT GCA AAC GCC TTC AAC AAC AGC ATT ATT	180	185	624
CCA GAA GAC ACC TTC TTC Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys	195	CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG	200	205	672
CTG GTC GAG AAA AGC TTT GAA ACA GAT ACG AAC CTA AAC TTT CAA AAC	210	215	220	Lys 720	720
Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn					
CTG TCA GTG ATT GGG TTC CGA ATC CTC CTC CTG AAA GTG GCC GGG TTT	225	230	235	Ile 768	768
Asn Leu Met Thr Leu Arg Leu Trp Ser Ser	240				821
GACAGCCTGT GCTCCCTCGC CCTTTCTCT GCATTGCCCT TCTTCTCCCT CTCCAAACAG					881
AGGGAACTCT CCTACCCCCA AGGAGGTGAA AGCTGCTACC ACCTCTGTGC CCCCCCGGCA					941
ATGCCACCAA CTGGATCTTA CCCGAATTAA TGATTAAGAT TGCTGAAGAG CTGCCAAACA					1001
CTGCTGCCAC CCCCTCTGTT CCCTTATTGC TGCTTGTCAC TGCTGACAT TCACGGCAGA					1061
GGCAAGGCTG CTGAGCCTC CCCTGGCTGT GCACATTCCC TCCTGCTCCC CAGAGACTGC					1121
CTCCGGCATC CCACAGATGA TGGATCTTCA GTGGGTTCTC TTGGGCTCTA GGTCTGGAG					1181

AATGTTGTGA GGGGTTTATT TTTTTTTAAT AGTGTTTCATA AAGA[REDACTED]ACA TAGTATTCTT
- CTTCTCAAGA CGTGGGGGAA [REDACTED]TTATCTCA TTATCGAGGC CCTGCTATGC TGTGTGTCTG
- GGCGTGTGT ATGTCCTGCT GCCGATGCCT TCATTTAAAT

1241

1301

1341

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
-18 -15 -10 -5

Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
1 5 10

Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
9 15 20 25 30

Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
35 40 45

Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe
50 55 60

Ala Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
65 70 75

Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg
80 85 90

Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile
95 100 105 110

Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser
115 120 125

Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val
130 135 140

Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu
145 150 155

Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser
160 165 170

Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile
175 180 185 190

Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys
195 200 205

Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn
210 215 220

Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Lys Val Ala Gly Phe
225 230 235

Asn Leu Leu Met Thr Ile Arg Leu Trp Ser Ser
240 245

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..933

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) POSITION: 1..63

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) POSITION: 64..933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG GAT ACC TGG CTC GTA TGC TGG GCA ATT TTT AGT CTC TTG AAA GCA Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala -21 -20 -15 -10	48
GGA CTC ACA GAA CCT GAA GTC ACC CAG ACT CCC AGC CAT CAG GTC ACA Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr -5 1 5 10	96
CAG ATG GGA CAG GAA GTG ATC TTG CGC TGT GTC CCC ATC TCT AAT CAC Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His 15 20 25	144
TTA TAC TTC TAT TGG TAC AGA CAA ATC TTG GGG CAG AAA GTC GAG TTT Leu Tyr Phe Tyr Trp Tyr Arg Gln Ile Leu Gly Gln Lys Val Glu Phe 30 35 40	192
CTG GTT TCC TTT TAT AAT AAT GAA ATC TCA GAG AAG TCT GAA ATA TTC Leu Val Ser Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe 45 50 55	240
GAT GAT CAA TTC TCA GTT GAA AGG CCT GAT GGA TCA AAT TTC ACT CTG Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu 60 65 70 75	288
AAG ATC CGG TCC ACA AAG CTG GAG GAC TCA GCC ATG TAC TTC TGT GCC Lys Ile Arg Ser Thr Lys Leu Glu Asp Ser Ala Met Tyr Phe Cys Ala 80 85 90	336
AGC AGC GAA ACT AAC TCC TAC GAG CAG TAC TTC GGG CCG GGC ACC AGG Ser Ser Glu Thr Asn Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg 95 100 105	384
CTC ACG GTC ACA GAG GAC CTG AAA AAC GTG TTC CCA CCC GAG GTC GCT Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala 110 115 120	432

C:\DOS\BIN\GCG4.0\BIN

GTC TTT GAG CCA TCA GCA GAG ATC TCC CAC ACC A AAG GCC ACA Val Phe Glu Pro Ser Gln Ala Glu Ile Ser His Thr Gln Lys Ala Thr 125 130 135	480
CTG GTG TGC CTG GCC ACA GGC TTC TAC CCC GAC CAC GTG GAG CTG AGC Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser 140 145 150 155	528
TGG TGG GTG AAT GGG AAG GAG GTG CAC AGT GGG GTC AGC ACA GAC CCG Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro 160 165 170	576
CAG CCC CTC AAG GAG CAG CCC GCC CTC AAT GAC TCC AGA TAC TGC CTG Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu 175 180 185	624
AGC AGC CGC CTG AGG GTC TCG GCC ACC TTC TGG CAG AAC CCC CGC AAC Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn 190 195 200	672
CAC TTC CGC TGT CAA GTC CAG TTC TAC GGG CTC TCG GAG AAT GAC GAG His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu 205 210 215	720
TGG ACC CAG GAT AGG GCC AAA CCT GTC ACC CAG ATC GTC AGC GCC GAG Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu 220 225 230 235	768
GCC TGG GGT AGA GCA GAC TGT GGC TTC ACC TCC GAG TCT TAC CAG CAA Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln 240 245 250	816
GGG GTC CTG TCT GCC ACC ATC CTC TAT GAG ATC TTG CTA GGG AAG GCC Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala 255 260 265	864
ACC TTG TAT GCC GTG CTG GTC AGT GCC CTC GTG CTG ATG GCC ATG GTC Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val 270 275 280	912
AAG AGA AAG GAT TCC AGA GGC TAG Lys Arg Lys Asp Ser Arg Gly 285 290	936

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 311 amino acids
 - (B) TYPE: amino acid
 - (C) TOPOLOGY: linear

- (ii) TYPE OF MOLECULE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala -21 -20 -15 -10
Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr -5 1 5 10
Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His 15 20 25

Leu Tyr Phe Tyr Trp [] Arg Gln Ile Leu Gly Gln [] Val Glu Phe
30 35 40

Leu Val Ser Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe
45 50 55

Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu
60 65 70 75

Lys Ile Arg Ser Thr Lys Leu Glu Asp Ser Ala Met Tyr Phe Cys Ala
80 85 90

Ser Ser Glu Thr Asn Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg
95 100 105

Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
110 115 120

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
125 130 135

Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
140 145 150 155

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
160 165 170

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
175 180 185

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
190 195 200

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
205 210 215

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
220 225 230 235

Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln
240 245 250

Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala
255 260 265

Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val
270 275 280

Lys Arg Lys Asp Ser Arg Gly
285 290

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
- (A) NAME/KEY: CDS

(B) POSITION: 1..39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGC CTC GTC CTT TCT GGT TCT GCA AGG CAA CTG ACC TTT
Cys Leu Val Leu Ser Gly Ser Ala Arg Gln Leu Thr Phe
295 300

39

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Cys Leu Val Leu Ser Gly Ser Ala Arg Gln Leu Thr Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) POSITION: 1..36
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TGC CTC GCT ACT GGT TCT GCA AGG CAA CTG ACC TTT
Cys Leu Ala Thr Gly Ser Ala Arg Gln Leu Thr Phe
15 20 25

36

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Cys Leu Ala Thr Gly Ser Ala Arg Gln Leu Thr Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGT GCC AGC AGT GGA ACA GAT TCC TAC GAG CAG TAC TTC
Cys Ala Ser Ser Gly Thr Asp Ser Tyr Glu Gln Tyr Phe
15 20 25

39

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Cys Ala Ser Ser Gly Thr Asp Ser Tyr Glu Gln Tyr Phe
1 5 10

21

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TGT GCC AGC AGT GAA ACA GAT TCC TAC GAG CAG TAC TTC
Cys Ala Ser Ser Glu Thr Asp Ser Tyr Glu Gln Tyr Phe
15 20 25

39

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Cys Ala Ser Ser Glu Thr Asp Ser Tyr Glu Gln Tyr Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO: 13.

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) POSITION: 1..39
 - xii) SEQUENCE DESCRIPTION: SEQ ID

TGT GCC AGC AGT GGA ACA GCT TCC TAC GAG CAG TAC TTC
 Cys Ala Ser Ser Gly Thr Ala Ser Tyr Glu Gln Tyr Phe
 15 20 25

30

(2) INFORMATION FOR SEO ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

Cys Ala Ser Ser Gly Thr Ala Ser Tyr Glu Gln Tyr Phe
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 15

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) POSITION: 1..39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15.

TGT GCC AGC AGT GGT ACA AAC TCC TAC GAG CAG TAC TTT
 Cys Ala Ser Ser Gly Thr Ash Ser Tyr Glu Gln Tyr Phe
 15 20 25

38

(2) INFORMATION FOR SEQ ID NO: 16

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

- (ii) TYPE OF MOLECULE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Cys Ala Ser Ser Gly Thr Asn Ser Tyr Glu Gln Tyr Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) POSITION: 1..39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TGT GCC ACC TCC GGG ACA GCT TCC TAC GAG CAG TAC TTC
Cys Ala Thr Ser Gly Thr Ala Ser Tyr Glu Gln Tyr Phe
15 20 25

39

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

- (ii) TYPE OF MOLECULE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Cys Ala Thr Ser Gly Thr Ala Ser Tyr Glu Gln Tyr Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) POSITION: 1..39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGT GCC AGA TCC GGG ACA GGC TCC TAC GAG CAG TAC TTC
Cys Ala Arg Ser Gly Thr Gly Ser Tyr Glu Gln Tyr Phe
15 20 25

39

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:..

Cys Ala Arg Ser Gly Thr Gly Ser Tyr Glu Gln Tyr Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO: 21:

- Q1
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single strand
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CACTGAAGAT CCATCATCTG

20

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single strand
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TAGAGGTGG TGGCAGACAG

20